1. (currently amended) A method for cloning one or more prokaryotic genes in a cassette array, the array being characterized by a plurality of genes where each gene is embedded in a predictable nucleotide sequence context including a repeat DNA sequence, the method comprising the steps of:

(a) hybridizing oligonucleotide primers to identified flanking repeat sequences in the cassette array;

(b) amplifying the DNA between the hybridized primers of step (a) to produce DNA fragments which contain one or more genes; and

(c) ligating the DNA fragments of step (b) into a vector for cloning, the one or more genes in a host cell.

2. (previously presented) The method of claim 1 wherein the one or more genes are selected from the group of peptides consisting of: adhesins, pilus proteins and outer membrane proteins; transporter peptides; toxins; hemolysins; hemagglutins; signaling peptides; detoxifying enzymes; catabolic enzymes specific for compounds episodically available, excluding compounds in the tricarboxylic acid cycle; and enzymes for biosynthesis of rare sugars, excluding ribose, deoxyribose; and sugars of the cell wall and the pericellular envelope.

3. (original) The method of claim 2 wherein said diversity-selected genes comprise restriction endonuclease genes.

4. (original) The method of claim 2 wherein said diversity-selected genes comprise methyltransferase genes.

5. (original) The method of claim 1 wherein said oligonucleotides contain recognition sites which permit directional cloning.

6. (original) The method of claim 5 wherein the DNA fragments are ligated into said vector in an orientation that enables expression.

7. (original) A method for identifying the presence of gene cassette arrays from within a target DNA preparation, said method comprising the steps of:

(a) hybridizing at least one oligonucleotide which hybridizes to one or more of SEQ ID NO:5 through SEQ ID NO:78 to a DNA preparation; and

(b) detecting the presence of a stable DNA-DNA hybrid.

8. (original) The method of claim 7 wherein said detection comprises determining the presence of stable DNA-DNA hybrid by Southern blot or dot blot.

9. (original) The method of claim 7 wherein said detection comprises employing at least two oligonucleotides and hybridizing said oligonucleotides to said DNA preparation, and detecting their ability to support DNA polymerization at the 3' end of the stable DNA-DNA hybrid.

10. (original) The method of claim 7 wherein said oligonucleotides comprise SEQ ID NO:79 through SEQ ID NO:91.

11. (original) The method of claim 7 wherein said oligonucleotides hybridize to one or more of DNA SEQ ID NO:5 through SEQ ID NO:78 or portions thereof.

12. (original) The method of claim 7 wherein the DNA source comprises an individual strain.

13. (original) The method of claim 7 wherein the DNA source comprises a group or pool of strains.

14. (original) The method of claim 7 wherein the DNA source comprises environmental DNA.

Claims 15-16 (cancelled).

17. (original) A method for identifying gene cassette arrays from a predetermined DNA sequence, said method comprising the steps of:

(a) screening the said predetermined DNA sequence for TAACWA;

(b) screening the said predetermined DNA sequence for CGTTRR;

(c) screening for DNA segments wherein the 5′ T of step A is less than about 200 base pairs form the 3′ R of step B; and

(d) determining whether the DNA sequence of step C is repeated in the predetermined DNA sequence.

18. (previously presented) The method of claim 2, wherein the adhesins are fimbrial proteins.

19. (previously presented) The method according to claim 2, wherein the signaling peptides are kinases.

20. (previously presented) The method according to claim 2, wherein the detoxifying enzymes are drug resistance determinants.